

Amendments to the claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of claims:

1. (Currently amended) A method for melanoma prognosis, comprising:
 - (a) isolating nucleic acid from a sentinel lymph node (SLN) sample obtained from a first melanoma patient;
 - (b) ~~amplifying nucleic acid targets from~~ mRNA transcripts encoded by a panel of marker genes from the nucleic acid from the SLN sample obtained from the first melanoma patient, wherein the panel comprises GalNAcT, PAX3, or both;
 - (c) ~~detecting the levels of the nucleic acid targets~~ mRNA transcripts encoded by the panel of marker genes in the nucleic acid from the SLN sample obtained from the first melanoma patient; and
 - (d) predicting metastatic melanoma recurrence, metastatic melanoma disease-free survival, overall survival, or a combination thereof, for the first melanoma patient based on the levels of the nucleic acid targets, wherein, as compared to ~~control~~ the levels of mRNA transcripts encoded by the panel of marker genes in nucleic acid from an SLN sample obtained from a second melanoma patient, an increase in the higher levels of the mRNA transcripts encoded by the panel of marker genes in the nucleic acid from the SLN sample obtained from the first melanoma patient indicate that the first melanoma patient has nucleic acid targets is indicative of an increased probability of metastatic in melanoma recurrence, a decreased probability of metastatic melanoma in disease-free survival, or a decreased probability of in overall survival, and a decrease in the lower levels of the mRNA transcripts encoded by the panel of marker genes in the nucleic acid from the SLN sample obtained from the first melanoma patient indicate that the

first melanoma patient has nucleic acid targets is indicative of a decreased probability of metastatic in melanoma recurrence, an increased probability of metastatic melanoma in disease-free survival, or an increased probability of in overall survival.

2. (Currently amended) The method of claim 1 wherein the panel further comprises marker genes selected from a group consisting of MAGE-A3, and MART-1, and Tyrosinase.

3. (Currently amended) The method of claim 2 wherein the panel comprises a first combination of MAGE-A3, GalNacT, MART-1, and PAX3; or a second combination of Tyrosinase, MART-1, GalNacT, and PAX3.

4. (Currently amended) The method of claim 1 wherein the nucleic acid is mRNA and the nucleic acid targets mRNA transcripts encoded by the panel of marker genes are amplified using real-time reverse transcriptase polymerase chain reaction (qRT-PCR).

5. (Previously presented) The method of claim 1 wherein the SLN sample is paraffin-embedded (PE) or frozen.

6. (Previously presented) The method of claim 1, wherein the SLN sample is histopathologically negative for melanoma cells.

7. (Previously presented) The method of claim 6, wherein histopathology of the SLN sample is determined by hematoxylin and eosin staining or immunohistochemistry.

8-9. (Canceled)

10. (Previously presented) The method of claim 1, wherein the patient's prognosis is predicted for at least a three-year period following a removal of a primary tumor, sentinel lymphadenectomy (SLND), or both.

11-30. (Canceled)

31. (Currently amended) A method for detecting the expression of a panel of marker genes in a patient, comprising:

- (a) obtaining a sentinel lymph node (SLN) sample from a melanoma patient, wherein the sample is histopathologically negative for melanoma cells;
- (b) isolating nucleic acid from the sample;
- (c) amplifying ~~nucleic acid targets from~~ mRNA transcripts encoded by a panel of marker genes from the nucleic acid from the SLN sample obtained from the melanoma patient, wherein the panel comprises GalNacT, PAX3, or both; and
- (d) detecting the levels of the ~~nucleic acid targets~~ mRNA transcripts encoded by the panel of marker genes.

32. (Currently amended) The method of claim 31 wherein the panel further comprises marker genes selected from a group consisting of MAGE-A3, and MART-1, and Tyrosinase.

33. (Currently amended) The method of claim 32 wherein the panel comprises a first combination of MAGE-A3, GalNacT, MART-1, and PAX3; or a second combination of ~~Tyrosinase~~, MART-1, GalNacT, and PAX3.

34. (Currently amended) A method for melanoma prognosis, comprising:

(a) isolating nucleic acid from a blood sample obtained from a first melanoma patient;

(b) ~~amplifying nucleic acid targets from~~ mRNA transcripts encoded by a panel of marker genes from the nucleic acid from the blood sample obtained from the first melanoma patient, wherein the panel comprises GalNAcT, PAX3, or both;

(c) detecting the levels of the ~~nucleic acid targets~~ mRNA transcripts encoded by the panel of marker genes in the nucleic acid from the blood sample obtained from the first melanoma patient; and

(d) predicting metastatic melanoma recurrence, metastatic melanoma disease-free survival, overall survival, or a combination thereof, for the first melanoma patient ~~based on the levels of the nucleic acid targets~~, wherein, as compared to ~~control~~ the levels of mRNA transcripts encoded by the panel of marker genes in nucleic acid from a blood sample obtained from a second melanoma patient, ~~an increase in the higher levels of the mRNA transcripts encoded by the panel of marker genes in the nucleic acid from the blood sample obtained from the first melanoma patient indicate that the first melanoma patient has nucleic acid targets~~ is indicative of an increased probability of metastatic in melanoma recurrence, a decreased probability of metastatic melanoma in disease-free survival, or a decreased probability of in overall survival, and a decrease in the lower levels of the mRNA transcripts encoded by the panel of marker genes in the nucleic acid from the blood sample obtained from the first melanoma patient indicate that the first melanoma patient has nucleic acid targets ~~is indicative of a decreased probability of metastatic in melanoma recurrence, an increased probability of metastatic melanoma in disease-free survival, or an increased probability of in overall survival.~~

35. (Currently amended) A method for melanoma prognosis, comprising:

(a) isolating nucleic acid from a non-sentinel lymph node (NSLN) sample obtained from a first melanoma patient;

(b) ~~amplifying nucleic acid targets from mRNA transcripts encoded by a~~
panel of marker genes from the nucleic acid from the NSLN sample obtained from the first melanoma patient, wherein the panel comprises GalNAcT, PAX3, or both;

(c) detecting the levels of the ~~nucleic acid targets~~ mRNA transcripts encoded by the panel of marker genes in the nucleic acid from the NSLN sample obtained from the first melanoma patient; and

(d) predicting metastatic melanoma recurrence, metastatic melanoma disease-free survival, overall survival, or a combination thereof, for the first melanoma patient ~~based on the levels of the nucleic acid targets~~, wherein, as compared to control the levels of mRNA transcripts encoded by the panel of marker genes in nucleic acid from an NSLN sample obtained from a second melanoma patient, an increase in the higher levels of the mRNA transcripts encoded by the panel of marker genes in the nucleic acid from the NSLN sample obtained from the first melanoma patient indicate that the first melanoma patient has nucleic acid targets is indicative of an increased probability of metastatic in melanoma recurrence, a decreased probability of metastatic melanoma in disease-free survival, or a decreased probability of in overall survival, and a decrease in the lower levels of the mRNA transcripts encoded by the panel of marker genes in the nucleic acid from the NSLN sample obtained from the first melanoma patient indicate that the first melanoma patient has nucleic acid targets is indicative of a decreased probability of metastatic in melanoma recurrence, an increased probability of metastatic melanoma in disease-free survival, or an increased probability of in overall survival.